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OM protein - protein search, using sw model
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perfect score:
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Listing first 45 summaries
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1189
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Goo B. Godzik A. Google C. seaber of the Bcl-2 family ",
Bcl-G. novel pro-spect C. seaber of the Bcl-2 family ",
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01-301-2001 (TEMBLES, 17, Created)
01-302-2001 (TEMBLES, 17, Last sequence undate)
APPTOSIS REGULATOR ELL-C SHORT POSM,
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Mammalla; Enteria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                           69.6%; Score 1189.5; DB 4: Length 252; 93.5%; Pred. No. 5.4e-88; Indels 7; Indels 7;
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*Functional annotation of a full-length mouse cDNA collection.";
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Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-JUN-2001 (FIRMURE) 17, Last Sequence update)
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"A detailed transcriptional map of the chromosome 12p12 tumor
suppressor locus,"
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Pred. No. 2.5e-87;
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EMBL: AK018579; BAB31290.1; --
EMBL: AK008682; BAB25830.1; --
BE SENDENCE FROM N.A. SOUR-THENES.

THE SENDLING-LINE AND SOUR-THENES.

THE MEDILING-LINE AND SHIPLE N. COROLD N. MARSH J. FANDE S.

THE MEDILING-LINE AND SHIPLE N. COROLD N. MARSH J. FANDE S.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09D3M3 2001 (TERMILFEL. 17, Created)
01-UNF-2001 (TERMILFEL. 17, Last sequence update)
01-UNF-2001 (TERMILFEL. 17, Last annotation update)
01-UNF-2001 (TERMILFEL. 17, Last annotation update)
01-UNF-2001 (TERMILFEL. 17, Last annotation update)
493140511 update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 FKSKEIFVTEGLSFOLOGHVPVASSSKKDEEBOILAKIVELLKYSGDOLERKLKKDKALM 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09 DIALI HILLIH 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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67.3%; Pred. No. 3.3e-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Mismatches
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Q9HB09

60 ВН 60

PRELIMINARY;

PRT;

334 AA

01-MAR-2001 (TERMELTEL. 16, Greated)
01-MAR-2001 (TERMELTEL. 16, Last sequence update)
01-MAR-2001 (TERMELTEL. 19, Last amountation update)
01-DE-2001 (TERMELTEL. 19, Last amountation update)
0201-2, SELATED PROLINE-RICH PROTEIN.

gukaryota Metazoa: Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalla; Butheria: Primates; Catarrhini; Hominidae; Homo.

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NCBI_TaxID=9606;

SEQUENCE FROM N.A. MEDLINE-21295042; PubMed-11401436;

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Matches Query Match Best Local Similarity

Conservative

22.9%;

67 WTEVSW---PCRNSQSSEKAINLGKKKSSWKAFFGVVEKEDSQSTPAKVSAGGORTLEYQ 123

43; Mismatches 118; Indels 58;

Score 124; DB 4; Length 334; pred, No. 0.053;

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Repurstional annexation of a full-length mouse cDMA collection.";
Repurstional annexation of a full-length mouse cDMA collection.";
Repurstional annexation of a full-length mouse collection.
Repurstic PSM 0502. 1974 BM. 1995—MARCHEST 1995—MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 PEPVENOSCENNOMERESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLESESVEORLE
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                                                                                                                                                                                                                                                                                                                                                                        235 GHEODGLSVSVEKTITDGVLMGVDPRGESBVKAOGFKAALVIDVTAKLTAIDNHOMNVL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 SKLKE-RVSETLYFREEG---FCDSKNKDGEDQIISKIVELLKFSGDOLGKEIKKDKALM 235
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                                                                                                                                                                                                                                                    236 SSFODGLSYSTEKTITDLFLRDYDTRGESEVKARGEKNALAIDATAKITAIDNHEMHEML 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 GFGTKYLREYPSPWVQQNGGWEKILGISHEEVD 328
                                                                                                                                295 GEGTKYLKENESPWIQQHGGWEKILGISHEEVD 327
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035844
                                         RESULT 8
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                                                                211 ----GTLAGLSVEHV-HSETPWIQAHGGWEGILAVS 241
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                                                                                              287 NHPMNRVLGFGTKYLKENFSPWIOOHGGWEKILGIS 322
                                                                                                                                       S
                                                                                                            156 -RESUDSFARIVELECSRUDSSRPSRACEGESPPSPEPLA----REALAMELSRRVAGIG 210
                                                                                                                                                                 113 ------ELGÓ------PESTEKEAILBRLVALLEEBAEVINOKLASDPALBSKLV 155
                                                                                                                                                                                      179 ELFYTBELISFOLOGHYPVASSSKKDEEDQILAKIVELLKYSGDOLERKLKKDKALMGHPQ 238
                                                                                                                                                                                                                                                    119 TLEYODSHSQQWSRCLSRVEGCLEHEAVDFKVISIANRVAEIVTSWFFFQATQAGGEKSK 178
                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAY-2001) to the ENBL/GenBank/DDBJ darabases.
ENBL: BC007724; ANU07724.1;
SEQUENCE 250 AN: 2887 MN; 61985F67DBF73664 CRc64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199516 PRELIMINARY: PRT; 230 AA.
01-002-2001 (Tremuscal. 19 Created)
01-002-2001 (Tremuscal. 19 Created)
01-002-2001 (Tremuscal. 19 Case Sequence update)
                                                                                                                                                                                                                                                                                 60 MCSA-NESWTEVSHPCRNSOSSEKALHLGKKKSSWKAFFGVVEKEDSOSTPAKVSAOGOR 118
                                                                                                                                                                                                                                                                                                                                                                    10 EEIFLJODDLATIEEKILAYYTRHHVENSTPALESPK-----LLKTRSLSORGLG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-UTERUS, AND LEIOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Romo seleters (Human).
Eukaryota; Mekazoa; Chordata; Crantata; Vertebrata; Euteleostomi;
Mammalia; Eutherta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         5 RELGIREDTL----RVIAAFLRRGENAGSPVPTPPRSPAQBEPTDFLSRLRRCLPCSLG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 SRRVAGLG----GTLAĞLSVEHV-HSFTPWİQAHGGHEGİLAVS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 TAKLTAIDNHPMNRVLGEGTKYLKENESPWIQOHGGWEKILGIS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 DPÅLRSKLV-RLŠSDSFARLVELFCSRDDSSRPSRACPGPFPFSPEPLA---RLALAMEL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 DKALMGHEODGISYSVEKTITDOVLMGVD-----PRGESEVKAQGEKNALVIDV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 VAQRUBQLVQBQLKSPPSPBLQG------PPSTEKENILRRLVALLBEBAEVINQKLAS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 GFKSKEIFVTEGL----SFOLOGHVFVASSSKKDEBEOILAKIVELLKYSGDOLERKLKK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 D-----FLSRLRRCLPGSLGRGAAPSESPRPGSLPIRPG---YGLEPGPÄTPDEYÄL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 DSHSQQWSRCLSNVEQCL-----EHEAVDPKVISTANKVAETVTSWPPPQAF---QAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 WRRRRWGPGPGASHAGSEB---LÄLREDTLRVLAAFLRRGEAAGSPVFTPPRSPAGEEPT 128
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 121; DB 4
20.2%; Pred. No. 0.062;
                                                                                                                                                                                                                                                                                                                                                                                                 44; Mismatches 102; Indels 122; Gaps
  PRT,
233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 250;
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                                                                   CASSAS.
                                                                                     035843
                                                                                                                                          179 EPWIQENGGWDTFVDL 194
                                                                                                                                                                       306 SPWIQQHGGWEKILGI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00452; Bc1-2;
Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR002475; BCL2_family.
InterPro: IPR000712; BCL2_family.
InterPro: IPR003033; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           035844;
                                                                      PRELIMINARY;
                                                                   PRT;
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В Ş Db

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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                           01-JAN-1998 (TERMBLrel. 05, Created)
01-JAN-1998 (TERMBLrel. 05, Last sequence update)
01-DEC-2001 (TERMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 EQVVNELFROGVN--WGRIVAFFSNGGALCVESVDKENOV---LVSRIASWNATTLADHL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 KTITDOYLM-GYDPRGESEYKAOGFKAALVIDYTAKLTAIDNHPMHRYLGFGTKYLKENF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 OCHYPVASSSKKDEEGQI-LAKIVELLKYSGDQLE---RKLKKDKALMGHFQDGLSYSVF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 -GH-----SSSIDAREVIPMAAVKOALREAGDEFELRYRRAFSDLTSGLHITFGTAYOSF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 SRCLSNVBOCLEHEAVDPKVISIANRVAEIVYSWEPPPOATOAGGEKSKEIFVTEGLSBOL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSOURMET FROM M. TESTIF-THYMES.
STAIL MEDICANS 1981 MANNED STRINGS.
FROM THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SOSHRELDVDPLSYKLSOKGYSHSQFSDVEENR----TEAPEETEAERETPSALNGNPSH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yakich 7.0% Score 119, D8 11; Length 233;
Local Similarity 27.3%, Pred. No. 0.002;
hes 54; Conservative 37; Mismarches 91; Indels 74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nis misculus (Mouse).
Bukaryona hekazoa: Ohordata, Craniata; Vertebrata; Buteleostomi;
Mummaila; Byingia: Rodentia; Schurgenathi; Muridhe: Murinne; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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IndesPeo; IRRODOTTS EGLZ_
INDESPeo; IRRODOTS EGLZ_
INDESPEO; IRRODOTS EGLZ_
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RRRRRRR OCCOORDED TO
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NCBL_TAXID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temnity 1622-035611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; score 117; DB 11; Length 235; Local similarity 21.8%; Pred. No. 0.12; Local similarity 21.8%; Pred. No. 0.12; hes 56; Conservative 35; Mismatches 88; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-ME-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 KTITDQVLM-GVDPRGESEVKAQGFKAALVIDVTAKLTAIDNHPMRVLGFGTKYLKENF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 QGHVPVASSSKKDEEEQI-LAKIVELLKYSGDQLE---RKLKKDKALMGHFQDGLSYSVF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 SOSSEKAI-----NLGKKKSSWKAFFGVVEKEDSOSTPAKVSAGGORTLEYODSHSOOW 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9QWX2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 EQVVNELFROGVN--WGRIVAFFSEGGALCVESVDKEMQV---LVSRIASWMATYLNDHL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata; Craniata; Yertebrata; Butaleostomi;
Hammailt, Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL-X (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 SPWIQQHGGWEKILGIS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 -GH-----SSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SQSNRELVVDFLSYKLSQKGYSNSQESDVEENR----TEAPEETEAERETPSAINGNPSW 57
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                                    WEDLINE J0330651; pubbed-10894153; per K U, Garrett L, Kubline J0330651; pubbed-10894153; per K U, Garrett L, Kubline J031061; per K U, Garrett L, Kubline J031061; per K U, Garrett L, Kubline J031061; per K U, Kubline J031061;
apoptosis during embryogenesis.
                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
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PS50063; BH4_2; 1
235 AA; 26122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1AF3
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Mol. Endocrinol. 14:1038-1052(2000).
EMEL. AROBSPOK: MAC 22372.11
HSSP: P39363; MS4171.
MSD: MSI STREAM ST. BELZ-2mily.
InterPro: P8000712; BcLZ-2.
Interpro: P8000712; BcLZ-2.
Interpro: P8000393; BH4.
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Pfam: PF02180; BH4: 1.
SMART: SM00337; BCL: 1.
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PROSITE: PS01080: BH1: 1.
PROSITE: PS01259: BH3: 1.
PROSITE: PS01259: BH4: 1.
PROSITE: PS01260: BH4_1: 1.
PROSITE: PS05063: BH4_2: 1.
PROSITE: PS05063: BH4_2: 1.
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                                                                 InterPro: IPROD2/5, BC/L2 family.
InterPro: IPROD2/13, BH.
InterPro: IPROD2/3,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSHING PRELIMINARY: PRT: 188 AA-
OSHING-2001 (TERMICAL-1.16, Circulus)
O1-MAR-2001 (TERMICAL-1.16, Circulus)
O1-MAR-2001 (TERMICAL-1.16, Lant unductation update)
O1-DEC-2001 (TERMICAL-1.18, 1 (ISOPOMM 1)) (FRADERT)-
MARAJJAGA-1.1 (CIRCULUS 1) (FRADERT)-
MARAJJAGA-1.1 (TROPOMM 1))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 SRCLSNVEOCLEHEAVDPKVISIANRVAEIVYSWPPEOATOAGGFKSKEIFVTEGLSFOL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 EPWIQENGGW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 SPWIQQHGGW 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nomo sepiens (Human)
Dukaryota: Metaroa: prinatas; craniata; Vertebrata; Buteleostomi;
Bukaryota: Metaroa: prinates; Catarriini; Hominidos, Homo.
Membalis; Matir-9606;
Membalis; Matir-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SOSNRELVVDFLSYKLSOKGYSWSOFSDVEENR----TEAPEETEAERETPSAINGNPSW 57
                                                                                                                                                                                                                                                                                                                                                                                                         Brown A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBLJ AL160175; CAC10003.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
PROSITE; PS01080; BH1;
                                         PROSITE; PS50062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GH----SSSLDAREVIPHAAVKOALREAGDEFELRYRRAFSDLTSGLHITFGTAYQSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Conservative
                                                                                                                                                                                                                                                                                                                                                                Q07817; 1LXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21126 MW; 4E62F8356D248E52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 116; DB 11; Length 188; 21.6%; Pred. No. 0.11; no. 1.21.
                                                         BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; Indels 74; Gaps
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                                                                                                                                              Db
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro IRPOUTING BULZ_family.
INTERPO IRPOUTING A. 2.
Fram: PROMSS; BOLZ_j. 1.
Fram: PROMSS; BOLZ_j. 1.
Fram: SHOUST; BOLZ_j.
Fram: BOURD BULZ_FAMILY, 1.
FRANCITE; BOLZ_SS BULZ_FAMILY, 1.
FRANCITE; FRANCISS BULZ_J.
NOW_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99N35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D
                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                          86 LGKKKSSNKAFFGYVEKEDSOSTFAKVSAOGORTLEYODSHSOOWSRGLSNVEGGLEHEA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBL/GenBank/DOBJ databases.
MMI, AF133281, AMXIS455.1,
HSSP, P55563 | AMXIS455.1,
HSSP, P55563 | AMXIS455.1,
The Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang X.-F., Cantor H.,
Sare Bolt CDM structure and genomic organization of apoptosis regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 20.9%
54: Conservative
                                                                1 LSOKGYSMSQFSDVEENR----TEAPEETEAERETPSAINGNPSW-------HLA 44
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-129/SVJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse),
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JBF-2001 (TrEMELTE1. 17, Created)
01-JBF-2001 (TrEMELTE1. 17, Last sequence update)
01-JBC-2001 (TrEMELTE1. 19, Last anotation update)
8-CELL LEUKENIA/LIMENOMA X (FRACKENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 ATYLNDHLEPWIQENGGW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 TKYLKENESPWIOOHGGW 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 PGTAYQSFEQWVNELFRUGVN--WGRIVAFFSFGGALCVESVDKEMQV---LVSRIAAWM 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 DGLSYSVFKTITDQVLM-GYDDRGESEVKAQGFKAALVIDVTAKLTAIDHHPMHRVLGFG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 TEGLSFOLOGHYPVASSSKKDEEROI-LAKIVELLKYSGDOLE---RKLKKDKALMGHEO 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ODSH9OOMSRCLSNVEQCLEHEAVDPKVISIANRVAEIVTSWPPPQATQAGGFKSKEIFV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 -NGAT----GH-----SSSLDAREVIEWAAVKOALREAGDEFELRYRNAFSDLTSOLHIT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50063; BH4_2; 1.
NON_TER 188 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 188 AA; 21029 MW; 7074B6095145G324 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 SOSSEKAI-----NIGKKKSSWKAFEGYVEK------EDSOSTFAKVSAOGORTLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SQSNRELIVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAING------ 53
                                                                                                                                                                                                                                                                                                                                                                   217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;
                                                                                                                                                                                           11arity 21.2%; Score 115; DB 11; Length 217; Conservative 34; Mismatches 88; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.78; Score 115; DB 4; Length 188; 20.9%; Pred. No. 0.13; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Mismatches 80; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 AA
                                                                                                                                              Ö
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                                                                                                                                                                                                                                                                        D<sub>D</sub>
                                                                                                                                                                                                                                                                                                                            5
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247 KTITDOVLM-GYDDRGESEVKAQGFKAALVIDVTAKLTAIDNHDWRVLGFGTKYLKENF 305
                                                                                                       191 OGHVPVAGSSKKDEEBQI-LAKIVELLKYSGDOLE---RKLKKDKALMGHEQDGLSYSVE 246
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DR R R R R R R R
                                                                                                                                                 Matches
                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
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                          131 SRCLSNVEQCLEHEAVDFKVISIANRVAEIVYSWFPPPQATQAGGEKSKEIFVTEGLSFQL 190
                                                                                                                                                                                          PROSITE: P801250; BH4_1; 1.
PROSITE: P830033; BH4_2; 1.
SEQUENCE 233 AA; 25047 MW; 2FA312818B25E17D CRC64;
                                                                                                                                                                                                                                          PROSITE; PS01258; BH2;
PROSITE; PS01259; BH3;
PROSITE; PS01260; BH4
77 SOSSEKAI-----HIGKKKSSHKAFEGYVEKEDSOSTPAKVSAOGORTLEYODSHSOOW 130
                                                                                                                                                                                                                                                                                    PROSITE: PS01080: BH1;
                                                                                                                                                                                                                                                                                                     PROSITE: PS50062;
                                                                                                                                                                                                                                                                                                                 SMART: SM00337; BCL,
SMART: SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00452; Bc1-2;
Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                    HSSP: 007817; IMAZ
InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; BCL2_family.
InterPro; IPR003093; BH4
                                                                                                                                           Watch 6.7%; Score 115; DB (Local Similarity 21.5%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                            Lee T.L., Canty J.M.;
"ere Cloning of a Porcine bcl-xL cDMA from Heart.";
Submitted (DE: 1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suls screta, (Pig).
Bidaryonea (Pig).
Mammalia: Butheria: Chordata: Craniata: Vertebrata: Buteleostomi;
Mammalia: Butheria: Cetartiodactyla; Sulma: Suldae: Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-007-2000 (TrBMG/rel. 15, Created)
01-007-2000 (TrBMG/rel. 15, Last sequence update)
01-007-2000 (TrBMG/rel. 19, Last sequence update)
AMTI_APOEPOTIC REGULATOR BCL_XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9MIA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 L 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 WORTVAFFSEGGALCVESVDKENOV---LVSRIASHNATYLNDHLEFWIGENOGNDTFVD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 GESBYKANGEFKAALVIDVTAKLTAIDHHEMNKYLGEGTKYLKENESEWIOOHGGWEKILG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 BQI-LAKIVELLKYSGDOLE---RKLKKDKALMGHFODGLSYSVEKTITDOVLM-GVDER 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 EVIPMAVKOALREAGDEFELRYRRAFSDLTSOLHITTFGTAYOSFEGVVNELFRDGVN-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 VDEKVISIANRVAEIVYSWEEPQATQAGGEKSKEIFVTBGLSEQLGGHVEVASSEKKDEE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 DSPAV----SSSLDAR 62
                                                                                                                Conservative 34; Mismatches 89; Indels 74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                            BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                              DB 6: Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA
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124 EQVVNELFRDÖÜN--WGRIYAFFSEGGALCVESVDKEMQV---LVSRIATWMATYLKDHL 178

69 TGH-----SSSLDAREVIPHAAVKQALREAGDEFELRYRRAFSDLTSGLHITPGTAYQSF 123

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RESULT 15
Q9UKN3
ID Q9UKN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                             Db
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         998
                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 6.7%; Score 115, DB 10; Length 562; Best Local Similarity 21.7%; Pred. No. 0.58; Matches 80; Conservative 43; Mismatches 136; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress). Subryophyta: Tracheophyta: Subaryota: Viridiplantae: Streptophyta: Subryophyta: Tracheophyta: Spermatophyta: Supolicophyta: audiooxy.deoms; core sudioox: Rosidae: gerosids III. Brassteales: Brassteaes: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSLAVO PRELIKINARY, PRT; 552 AA.
OSLAVO) 100 (TREMICHA) 1.5 (Created)
0.007.2000 (TREMICHA) 1.5 (Last sequence update)
0.007.2000 (TREMICHA) 1.5 (Last sequence update)
MIRFORHETICAL 63.3 KDA PROTEIN.
T24118_70;
09UKN3 PRELIMINARY; PRT; 386 AA.
09UKN3;
01-MAY 2000 (TIEMBLIFE! 13, Created)
01-MAY 2000 (TIEMBLIFE! 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ED Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL, ALS39013; CAB8234.1; -
Hypothetical protein
SEQUENCE 562 AN; 63328 MH; CFDB35EC6ED529F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bevan M., Robben J., Grymonprez B., Volkkaert G., Bancroft I.,
Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.:
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 EPWIQENGGWD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 SPWIQQHGGWE 316
                                                                                                                                                                                                           466 NWTRPWSEQ 474
                                                                                                                                                                                                                                                            307 ---- PWIQQ 311
                                                                                                                                                                                                                                                                                                                                                             359 STLIGNINTL-LQPHNLSFTSKYSKIIQYHLEAIISQSVYQDFENCVFQKNGKPKLLDPE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 QILAKIVELLKYSGDQLERKLKKDKALMGHFQDGLSYSVFKTITDQVLMG------VDPR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 ---- SQENSGGRSSGKKNSEMPVSE--EVMVEGFLQIVSEARLSIKQFLKTLVSEIDEED 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 SGVEKLKRELMEANRSRDAALTQVSEMKSSLGELSEKLQYLESYCDNLKKALREATEVV- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 -PLTDSHSAVVSSQPRNRGGRVMSWLFPKLKKKQKSNSIFNSPSITEKSEEVSEVLKDSG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 WPCRNSQS---SEKAINLG------KKKSSWKAFF---GVVEKEDSQSTPAKVSA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWPPPQATQAG---GPKSKEIFVTEGLSPQLQGHVPVASS-----SKKDEEE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGQRTLEYQ------DSHSQQWSRCLSNVEQCLEH----EAVDPKVISIANRVAEIVY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHHHVYTMSDALRSPPLHFYTTGRSNCGSVDFRSVSSCNDYNKQXGFDTKSLXSSNLVV- 186
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Matches
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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